

Gencore version 4.5
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OM protein - protein search, using sw model

Run on: March 1, 2001, 16:16:47 ; Search time 91.75 Seconds
(without alignments)

Sequence: 24.287 Million cell updates/sec

Title: US-09-331-631A-5_COPY_76_144

Perfect score: 381
Score: 1 NRQDPQQYEQCOKRCQRR..... EEQOREDEEKEYEERMKEDN 69

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39; *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	RESULT	1
1	145.5	38.2	588	1	VCIB_GOSHI	ID VCIB_GOSHI	
2	128	33.6	605	1	VCIB_GOSHI	STANDARD; PRY; 588 AA.	
3	103	27.0	1898	1	TRHY_RABIT	AC P09801; DT 01-MAR-1989 (Rel. 10, Created)	
4	103	26.2	1407	1	TRHY_RABIT	DT 01-MAR-1989 (Rel. 10, Last sequence update)	
5	97.5	25.6	877	1	INNE_CHICK	DT 15-JUL-1999 (Rel. 38, Last annotation update)	
6	97	25.5	482	1	U2R2_HUMAN	DE VICTILIN C72 PRECURSOR (ALPHA-GLOBULIN B).	
7	92.5	25.1	1023	1	GLT_DROME	OS Gossypium hirsutum (Upland cotton).	
8	95	24.9	524	1	SBP_SOYBN	OC Eukaryota; Embryophyta; Tracheophyta; spermatophyta; Magnoliophyta; eudicots; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.	
9	95	24.9	905	1	SNF5_YEAST	OC Malvales; Malvaceae; Gossypium.	
10	94	24.7	648	1	KAPC_DICID	CC RY	
11	94	24.7	1085	1	YAFR_SCHPO	CC RY	
12	93	24.4	129	1	APAL_MACPA	CC RY	
13	93	24.4	2124	1	Y192_HUMAN	CC RY	
14	92.5	24.3	103	1	PRO_DROME	CC RY	
15	91.5	24.0	573	1	GLBL_MATE	CC RY	
16	90	23.6	678	1	GARP_PLAIF	CC RY	
17	90	23.5	1344	1	IT3R_MOUSE	CC RY	
18	89.5	23.5	758	1	YMB8_YEAST	CC RY	
19	89	23.4	285	1	INVO_CANEPA	CC RY	
20	89	23.4	1382	1	IF3B_HUMAN	CC RY	
21	88	23.1	1157	1	Y182_HUMAN	CC RY	
22	88	23.1	1905	1	TAGB_DICOI	CC RY	
23	87.5	23.0	538	1	C111_YEAST	CC RY	
24	87.5	23.0	1549	1	TRH1_SHEEP	CC RY	
25	87.5	22.4	550	1	BLSA_HUMAN	CC RY	
26	85.5	22.4	572	1	MOES_LYVIA	CC RY	
27	85.5	22.4	695	1	XET_HUMAN	CC RY	
28	84.5	22.2	47	1	AGRP_LURCY	CC RY	
29	84	22.0	1240	1	YNT1_YEAST	CC RY	
30	83.5	21.9	466	1	CYP9_CAEEL	CC RY	
31	83.5	21.9	471	1	RUI7_XENIA	CC RY	
32	83	21.8	479	1	U2RL_HUMAN	CC RY	
33	82.5	21.7	444	1	CEB_DROME	CC RY	
					SEQUENCE 588 AA; 69729 MW; 63E69B29AB8ADEB CRC64;	SEQUENCE 588 AA; 69729 MW; 63E69B29AB8ADEB CRC64;	SEQUENCE 588 AA; 69729 MW; 63E69B29AB8ADEB CRC64;
					FT SIGNAL 1	FT SIGNAL 1	FT SIGNAL 1
					SEQUENCE 26	SEQUENCE 26	SEQUENCE 26
					KN SIGNAL 25	KN SIGNAL 25	KN SIGNAL 25
					DR SIGNAL	DR SIGNAL	DR SIGNAL
					DR PRFAM; PR00546; Seedstore 7's; 1.	DR PRFAM; PR00546; Seedstore 7's; 1.	DR PRFAM; PR00546; Seedstore 7's; 1.
					DR KN	DR KN	DR KN
					DR FT	DR FT	DR FT
					DR SIGNAL	DR SIGNAL	DR SIGNAL
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DR HSSP; P21836; 1MAR.
 DR FLYBASE; FBgn001114; Glt.
 DR INTERPRO; IPR002018; -.
 DR PFAM; PF00135; Coesterase; 2.
 DR PROSITE; PS00941; CARBOXYLESTERASE_B-2; 1.
 KW Glycoprotein; Sulfatase; Calcium-binding; Signal.
 FT SIGNAL 1 17
 FT CHAIN 18 1023 GLUTACTIN.
 FT SIMILAR 18 602 WITH TYPE-B CARBOXYLESTERASE/LIPASES.
 FT DOMAIN 603 615 POLY-THR.
 FT DOMAIN 616 1023 GLU/GLN-RICH.
 FT CARBOHYD 115 115 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 368 368 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 810 810 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 123 145 BY SIMILARITY.
 FT DISULFID 298 315 BY SIMILARITY.
 SQ SEQUENCE 1023 AA; 118412 MW; 3630CF79AB86058C CRC64;
 SQ 731 QQEREQREELRRQQREEQEQPE 759

Query Match 25.1%; Score 95.5%; DB 1; Length 1023;
 Best Local Similarity 32.6%; Pred. No. 0.37; Gaps 3;
 Matches 29; Conservative 17; Mismatches 20; Indels 23; Gaps 3;

Db QY 1 NRQDPQ-----QEQCQCORRETERPHMQ-----ICQRCRERYEKE 41
 671 DQQRQPYQQPREQQQDERIQQREQERLQQREQEQERLQQREQEQERE 730

Qy 42 KRKQKQR-----IEQQQDEEYVEERKE 66

Db 731 QQEREQREELRRQQREEQEQPE 759

RESULT 8

SBP_SOBN STANDARD; PRT; 524 AA.

ID SBP_SOBN STANDARD; PRT; 524 AA.

AC Q04672; 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)

DE SUCROSE-BINDING PROTEIN PRECURSOR (SBP).
 GN SBP.
 OS Glycine max (Soybean).
 OC Fabaceae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicots; core eudicots; Rosidae; eurosids I;
 OC Fabales; Papilionoideae; Glycine.
 RN [1]
 SEQUENCE FROM N.A., AND SEQUENCE OF 30-50.

PTISSUE-EMBRYO;
 RX MEDLINE=93104680; PubMed=1467654;
 RA Grimes H.D., Overvoorde P.J., Ripp K., Franceschi V.R., Hitz W.D.;
 RT "A 62-kD sucrose binding protein is expressed and localized in
 tissues actively engaged in sucrose transport.";
 RL Plant Cell 4:1561-1574(1992).
 "-!- FUNCTION: PLAYS A ROLE IN SUCROSE TRANSPORT.
 CC -!- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED.

-!- TISSUE SPECIFICITY: ASSOCIATED WITH THE PLASMA MEMBRANE OF
 SEVERAL CELL TYPES ENGAGED IN SUCROSE TRANSPORT, INCLUDING THE
 MESOPHYLL CELLS OF YOUNG SINK LEAVES, THE COMPANION CELLS OF
 MATURE PHLOEM AND THE CELLS OF DEVELOPING COTYLEDONS.

-!- DEVELOPMENTAL STAGE: IN THE COTYLEDON, EXPRESSION IS NOT DETECTED
 UNTIL 10 DAYS AFTER FERTILIZATION, BETWEEN 10-19 DAYS AFTER
 FERTILIZATION, EXPRESSION INCREASES RAPIDLY BUT DECLINES 20-30
 DAYS AFTER FERTILIZATION. 30 DAYS AFTER FERTILIZATION, NO
 EXPRESSION OCCURS. THIS EXPRESSION PATTERN CLOSELY PARALLELS THE
 RATE OF SUCROSE UPTAKE IN THE COTYLEDON.

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CC EMBL; L06038; AA03894.1; -.

DR PIR; J01730; J01730.

DR ISSN; P50477; ICAN.

DR INTERPRO; IPR00113; -.

DR PFAM; PF0056; Seedstore_7s; 1.

FT SIGNAL 1 29 TRANSPORT; Sugar transport; Signal; Membrane.

FT CHAIN 30 524 AA; 60522 MW; 0251EE90756EF341 CRC64;

Query Match 24.9%; Score 95%; DB 1; Length 524;
 Best Local Similarity 35.9%; Pred. No. 0.22; Gaps 3;
 Matches 23; Conservative 16; Mismatches 15; Indels 10; Gaps 3;

Db QY 12 QQQKCORRETERPHMQICQRCR--RYEKKRKQ----QKRYEQQRDRBEEKYEERM 64
 46 QQQQQQQTYEDKRR--VCIOSCDRTHRMKQREKQIQQEEETREKKEESRREEEQEOH 102

RESULT 9

SNF5_YEAST STANDARD; PRT; 905 AA.

ID SNF5_YEAST STANDARD; PRT; 905 AA.

AC P0480; 01-OCT-1990 (Rel. 16, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE TRANSCRIPTION REGULATORY PROTEIN SNF5 (SNF/SNF COMPLEX COMPONENT SNF5)
 DE (TRANSCRIPTION FACTOR TYPE).
 SNF5 OR TYE4 OR SWI10 OR YBR289W OR YBR2036.

GN SNF5_YEAST STANDARD; PRT; 905 AA.

OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetales;
 OC Saccharomycetaceae; Saccharomyces.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MCY;

RX MEDLINE=91042489; PubMed=2233708;
 RA Laurent C., Treitel M.A., Carlson M.;
 RT "The SNF5 protein of *Saccharomyces cerevisiae* is a glutamine- and
 proline-rich transcriptional activator that affects expression of a
 broad spectrum of genes.";
 RT Mol. Cell. Biol. 10:616-5625(1990).
 RL [2]
 RP SEQUENCE FROM N.A.

CC MEDLINE=94378722; PubMed=8091861;
 CC MLLDLINE=94378722;
 RT Holmsrom K., Brandt T., Kallese T.;
 RT "The sequence of a 32,420 bp segment located on the right arm of
 chromosome II from *Saccharomyces cerevisiae*";
 RL Yeast 10:547-562(1994).
 CC COMPLEX IS REQUIRED FOR THE INDUCED EXPRESSION OF A LARGE NUMBER
 OF GENES. THIS COMPLEX ALTERS CHROMATIN STRUCTURE TO FACILITATE
 BINDING OF GENE-SPECIFIC DEDICATED TRANSCRIPTION FACTORS.

-!- SUBUNIT: COMPONENT OF THE SWI/SNF GLOBAL TRANSCRIPTION ACTIVATOR
 CC COMPLEX.
 CC -!- SUBCELLULAR LOCATION: NUCLEAR.
 CC -!- SIMILARITY: BELONGS TO THE SNF5 FAMILY.

CC -----

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 or send an email to license@isb-sib.ch).

CC -----

RP SEQUENCE FROM N.A.
 RC STRAIN-CV. INBRED LINE VA26;
 RA Belanger F.C.; Kriz A.L.;
 RT "Molecular characterization of the major maize embryo globulin encoded
 by the Glb1 gene.",
 RL Plant Physiol. 91:636-643(1989).
 RN [2]
 RP SEQUENCE OF 87-100.
 RX MEDLINE:89374022; PubMed=2775172;
 RA Kriz A.L.;
 RT "Characterization of embryo globulins encoded by the maize Glb
 genes.",
 RL Biochem. Genet. 27:239-251(1989).
 CC -!- PTM: THREE PROTEIN PROCESSING STEPS OCCUR IN THE FORMATION OF THE
 CC MATURE PROTEIN FROM THE PRIMARY TRANSLATION PRODUCT.
 CC -!- POLYMORPHISM: THE THREE MOST COMMONLY OCCURRING GLB1 ALLELES HAVE
 CC THE DESIGNATION L, I, AND S FOR LARGE, INTERMEDIATE, AND SMALL
 CC PROTEINS, RESPECTIVELY.
 CC -!- SIMILARITY: TO OTHER 7S SEED STORAGE PROTEINS (PHASOLIN, VICILIN,
 CC CONVICILIN, CONGLICININ, ETC.).
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 DR EMBL; M24845; AAA33467.1; -.
 DR HSSP; P50477; ICW.
 DR MATZEDB; 30181; -.
 DR INTERPRO; IPR00113; -.
 DR PFAM; PF00446; Seedstore_7s; 1.
 KW Seed storage protein; Signal.
 FT SIGNAL 1 18 OR 21 (POTENTIAL).
 FT PROPEP 19 86 GLOBULIN-1 S ALLELE.
 FT CHAIN 87 573 N-LINKED (GLCNAC, .) (POTENTIAL).
 FT CARBOHD 349 573 AA; 65029 MW; 525ED1D0A062976 CRC64;
 SQ

Query Match 24.0%; Score 91.5; DB 1; Length 573;
 Best Local Similarity 33.3%; Pred. No. 0 47;
 Matches 22; Conservative 16; Mismatches 13; Indels 15; Gaps 4;
 Oy 12 QCQKRCORRETERPRHMQ-ICQORCERYEKKRKQKRYE-----EQOREDEEKY 60
 Db 39 RCVRRCEDR--PWHQRPRCLEQK-RBEERERQRERSHEADRSSEGSSBEDEREREQK 94
 Oy 61 EERMEK 66
 Db 95 EEKQKD 100

Search completed: March 1, 2001, 16:16:49
 Job time: 429 sec

